## ABSTRACT

Disclosed are methods and systems for applying independent component analysis (ICA) and other advanced signal processing techniques to automatically identify an optimal number of independent gene clusters and to efficiently separate gene expression data into biologically relevant groups. Embodiments of the methods and systems of the present invention provide an interface that allows the user to review the results at various stages during the analysis, thereby optimizing the type of analysis performed for a specific experiment. Also disclosed are methods and systems to mathematically define the relationship for gene expression within a group of interrelated genes.